

To Study the Microbiological Profile and Antimicrobial Susceptibility Pattern of Vaginal Infections Among Women Attending A Tertiary Care Gynecology Clinic

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Abstract

Background: Vaginal infections are among the common causes of gynecological morbidity and may present with vaginal discharge, itching, burning, irritation, foul odor, dysuria and dyspareunia. The etiological spectrum is diverse and includes bacterial, fungal and protozoal organisms. Since the clinical manifestations of different vaginal infections frequently overlap, microbiological

evaluation is important for establishing the etiological diagnosis and guiding appropriate treatment.

Aim: To study the microbiological profile and antimicrobial susceptibility pattern of vaginal infections among women attending a tertiary-care gynecology clinic.

Materials and Methods: A prospective observational study was conducted among 85 women presenting with

symptoms suggestive of vaginal infection. Relevant demographic and clinical information was recorded. Vaginal specimens were collected under aseptic precautions and subjected to direct microscopic examination and culture using standard microbiological procedures. Antimicrobial susceptibility testing was performed for clinically significant bacterial isolates using standard laboratory methods.

Results: Among the 85 women studied, 22 (25.9%) showed microbiological evidence of vaginal infection, whereas 63 (74.1%) had no significant pathogen detected. Vaginal discharge was the predominant symptom, reported by 78 (91.8%) participants, followed by vaginal itching in 52 (61.2%) and foul-smelling discharge in 38 (44.7%). White or whitish discharge was the commonest type of discharge.

Conclusion: Vaginal infections demonstrate considerable clinical and microbiological diversity. The findings emphasize the importance of appropriate microbiological evaluation in symptomatic women and rational antimicrobial use based on laboratory findings.

Keywords: Vaginal Infection; Vaginitis; Candida; Bacterial Vaginosis; Escherichia Coli; Trichomonas Vaginalis; Antimicrobial Susceptibility.

Introduction

Vaginal infections are among the most frequent causes of gynecological morbidity and represent an important public-health problem. Women with vaginal infections commonly present with abnormal vaginal discharge, itching, burning, irritation, unpleasant odor, dysuria and dyspareunia. Although these symptoms may suggest an infectious etiology, clinical manifestations frequently overlap between different causes, making an etiological diagnosis based solely on symptoms unreliable¹⁻³.

The normal vaginal environment is characterized by a dynamic microbial ecosystem in which Lactobacillus species play an important protective role. Lactobacilli contribute to maintenance of an acidic vaginal pH and inhibit the growth and colonization of potentially pathogenic microorganisms. Disturbance of this microbial equilibrium may result in vaginal dysbiosis and predispose women to symptomatic vaginal disorders^{4,5}.

Bacterial vaginosis (BV) is one of the common causes of vaginal discharge. It is characterized by replacement of the normal Lactobacillus-dominant microbiota by a polymicrobial community containing anaerobic organisms and other bacterial species, particularly Gardnerella vaginalis. The clinical presentation may include thin, homogeneous discharge and characteristic odor, although symptoms are variable⁶⁻⁸.

Vulvovaginal candidiasis (VVC) is another important cause of vaginitis. Candida albicans accounts for the majority of cases, while non-albicans Candida species such as Candida glabrata and Candida tropicalis may also be involved. Typical manifestations include vulvovaginal itching, soreness, external dysuria, dyspareunia and abnormal discharge^{9,10}.

Trichomoniasis, caused by Trichomonas vaginalis, is an important sexually transmitted infection. It may cause vaginal discharge, vulvovaginal irritation and dysuria. However, a considerable proportion of infected women may have minimal or no symptoms, emphasizing the importance of laboratory diagnosis^{11,12}.

Aerobic bacterial organisms may also contribute to symptomatic vaginal infection. Organisms such as Escherichia coli, Staphylococcus aureus, Enterococcus species and other aerobic bacteria have been described in association with aerobic vaginitis. Aerobic vaginitis

differs from bacterial vaginosis and may require different clinical and microbiological assessment^{13,14}.

The clinical overlap among bacterial vaginosis, vulvovaginal candidiasis, trichomoniasis and aerobic bacterial infections creates diagnostic challenges. Vaginal pH assessment, microscopy, Gram staining, culture and molecular diagnostic methods may assist in establishing the correct diagnosis.^{1,3,15}

Microscopy remains an important and relatively inexpensive diagnostic method, particularly in resource-limited settings. Culture can provide additional information regarding bacterial and fungal pathogens and is particularly useful in recurrent, persistent or atypical infections. Molecular methods have increasingly become available and may provide greater sensitivity for selected pathogens^{15,16}.

Antimicrobial resistance represents another important challenge in the management of bacterial vaginal infections. Repeated empirical treatment and inappropriate antimicrobial exposure may contribute to the selection of resistant organisms. Antimicrobial susceptibility testing can therefore help guide treatment and promote antimicrobial stewardship^{17,18}.

The prevalence and etiological spectrum of vaginal infections vary between geographical regions and patient populations. Differences may be related to age, pregnancy status, sexual behavior, hygiene practices, previous antimicrobial exposure, diagnostic methodology and healthcare-seeking patterns. Consequently, local microbiological surveillance is important for understanding the organisms responsible for symptomatic vaginal infections and their susceptibility profiles.

Recent studies have further emphasized the complexity of the vaginal microbiome and the potential value of molecular diagnostics. Modern molecular techniques can

identify multiple organisms simultaneously and may improve differentiation between bacterial vaginosis, candidiasis and trichomoniasis. However, detection of an organism does not always equate to clinically significant disease, and laboratory findings should be interpreted together with clinical features¹⁹⁻²⁶.

Therefore, the present study was undertaken to assess the microbiological profile of vaginal infections among women attending a tertiary-care gynecology clinic and to evaluate antimicrobial susceptibility among clinically significant bacterial isolates.

Materials and Methods

Study Design and Setting

A prospective observational study was conducted among women attending the gynecology clinic of a tertiary-care hospital with symptoms suggestive of vaginal infection.

Study Population

A total of 85 women presenting with symptoms suggestive of vaginal infection were included in the study. Demographic and clinical information was recorded using a structured proforma.

Inclusion Criteria

1. Women presenting with symptoms suggestive of vaginal infection, particularly abnormal vaginal discharge.
2. Women willing to participate in the study.
3. Women willing to provide vaginal specimens.
4. Patients attending the gynecology clinic during the study period.

Exclusion Criteria

5. Women who had received antimicrobial or antifungal treatment shortly before specimen collection.
6. Women unwilling to participate or unwilling to provide samples.

7. Patients with inadequate or improperly collected specimens.
8. Patients with conditions likely to interfere with microbiological assessment.

Sample Collection

After obtaining appropriate informed consent, vaginal specimens were collected using sterile vaginal swabs under aseptic precautions. Relevant clinical findings, including the character of vaginal discharge, itching, burning, odor, dysuria, lower abdominal pain and dyspareunia, were recorded. Specimens were transported promptly to the microbiology laboratory for processing.

Microbiological Examination

The collected vaginal specimens were subjected to direct microscopic examination and culture using standard microbiological procedures. Direct microscopy was performed for detection of fungal elements, protozoal organisms and other relevant findings. Culture was performed using appropriate culture media, followed by identification of bacterial and fungal isolates using standard laboratory techniques.

Antimicrobial Susceptibility Testing

Antimicrobial susceptibility testing was performed for clinically significant bacterial isolates using the Kirby–Bauer disk diffusion method on Mueller–Hinton agar. Isolates were interpreted as sensitive, intermediate or resistant according to applicable laboratory interpretative criteria.

Data Collection and Statistical Analysis

Demographic, clinical and microbiological findings were recorded and analyzed descriptively. Categorical variables were expressed as frequencies and percentages. The total study population consisted of 85 cases.

Results

A total of 85 women were included in the present study. The age distribution showed that the largest proportion of participants belonged to the 31–40-year age group, comprising 29 (34.1%) women, followed by the 21–30-year group with 27 (31.8%). Seventeen (20.0%) participants were aged 41–50 years, while 7 (8.2%) were older than 50 years and 5 (5.9%) were aged ≤ 20 years.

Table 1: Age wise distribution

Age group (years)	Number (n)	Percentage (%)
≤ 20	5	5.9
21–30	27	31.8
31–40	29	34.1
41–50	17	20.0
>50	7	8.2
Total	85	100.0

Vaginal discharge was the predominant presenting symptom and was reported by 78 (91.8%) women. Vaginal itching was reported by 52 (61.2%), foul-smelling discharge by 38 (44.7%), vaginal burning by 29 (34.1%), lower abdominal pain by 24 (28.2%), dysuria by 19 (22.4%) and dyspareunia by 15 (17.6%). Multiple symptoms were present in several participants.

Table 2: Presenting Symptoms

Presenting symptom	Number (n)	Percentage (%)
Vaginal discharge	78	91.8
Vaginal itching	52	61.2
Foul-smelling discharge	38	44.7
Vaginal burning	29	34.1
Lower abdominal pain	24	28.2
Dysuria	19	22.4
Dyspareunia	15	17.6

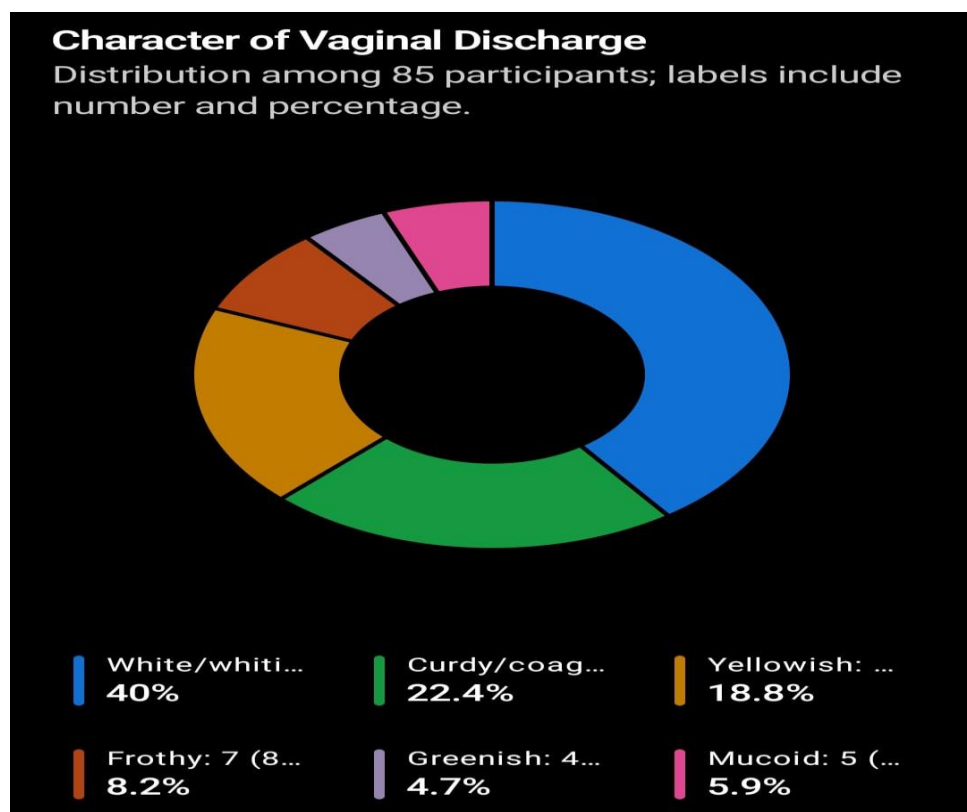
Regarding the character of vaginal discharge, white or whitish discharge was the most frequent type, occurring in 34 (40.0%) women. Curdy or coagulated discharge was

observed in 19 (22.4%), yellowish discharge in 16 (18.8%), frothy discharge in 7 (8.2%), greenish discharge in 4 (4.7%) and mucoid discharge in 5 (5.9%).

Table 3: Character of discharge

Character of discharge	Number (n)	Percentage (%)
White/whitish	34	40.0
Curdy/coagulated	19	22.4
Yellowish	16	18.8
Frothy	7	8.2
Greenish	4	4.7
Mucoid	5	5.9
Total	85	100.0

Graph 1: Characteristics of Vaginal discharge



On microbiological examination, 22 of the 85 participants (25.9%) were positive for infection, while 63 (74.1%) had no significant pathogen detected. Thus, approximately one-fourth of symptomatic women demonstrated microbiological evidence of infection.

Table 4: Outcome

Overall outcome	Number (n)	Percentage (%)
Positive for infection	22	25.9
No significant pathogen detected	63	74.1
Total	85	100.0

Table 5: Proposed Antimicrobial Susceptibility Pattern Among Bacterial Isolates

Bacterial isolate	No.	Amikacin (%)	S Ampicillin (%)	S Ceftriaxone (%)	S Ceftazidime (%)	S Ciprofloxacin (%)	S Gentamicin (%)	S Meropenem (%)	S Imipenem (%)
E. coli	7	6 (85.7)	2 (28.6)	4 (57.1)	4 (57.1)	4 (57.1)	5 (71.4)	7 (100)	7 (100)
Klebsiella spp.	4	4 (100)	1 (25.0)	3 (75.0)	3 (75.0)	2 (50.0)	3 (75.0)	4 (100)	4 (100)
S. aureus	4	3 (75.0)	2 (50.0)	3 (75.0)	3 (75.0)	3 (75.0)	3 (75.0)	4 (100)	4 (100)
Enterococcus spp.	3	2 (66.7)	2 (66.7)	1 (33.3)	1 (33.3)	2 (66.7)	2 (66.7)	2 (66.7)	2 (66.7)
Pseudomonas spp.	2	2 (100)	—	1 (50.0)	2 (100)	1 (50.0)	2 (100)	2 (100)	2 (100)
Total	20	17 (85.0)	7 (35.0)	12 (60.0)	13 (65.0)	12 (60.0)	15 (75.0)	19 (95.0)	19 (95.0)

E. coli was the most frequently represented organism, with 7 isolates. Susceptibility was highest to meropenem and imipenem (100%), followed by amikacin (85.7%) and gentamicin (71.4%). Ampicillin showed the lowest susceptibility (28.6%).

- Klebsiella spp. accounted for 4 isolates. All isolates were susceptible to amikacin, meropenem and imipenem (100%), while susceptibility to ampicillin was low (25%).
- Staphylococcus aureus comprised 4 isolates. Susceptibility was highest to meropenem and imipenem (100%), while ampicillin showed 50% susceptibility.
- Enterococcus spp. included 3 isolates. Susceptibility varied between antibiotics, with ampicillin and ciprofloxacin showing 66.7% susceptibility, while ceftriaxone and ceftazidime showed 33.3%.

- Pseudomonas spp. comprised 2 isolates. Both were susceptible to amikacin, ceftazidime, gentamicin, meropenem and imipenem (100%), whereas ciprofloxacin showed 50% susceptibility.

Discussion

The present study was undertaken to evaluate the microbiological profile and antimicrobial susceptibility pattern of vaginal infections among women attending a tertiary-care gynecology clinic. A total of 85 symptomatic women were included, of whom 22 (25.9%) demonstrated microbiological evidence of infection, while 63 (74.1%) had no significant pathogen detected. The findings demonstrate that although vaginal symptoms are frequent among women attending gynecology clinics, microbiological confirmation of infection may occur in only a proportion of symptomatic patients. This observation highlights the importance of appropriate

clinical assessment supported by laboratory investigation rather than relying exclusively on symptoms.

In the present study, the majority of women belonged to the 31–40-year age group (34.1%), followed by those aged 21–30 years (31.8%). The predominance of women in the reproductive-age groups is clinically relevant because hormonal influences, sexual activity, pregnancy-related changes, antimicrobial exposure and alterations in vaginal microbiota may influence susceptibility to vaginal disorders. Similar observations have been reported in previous studies in which symptomatic vaginal infections were predominantly encountered among women of reproductive age^{1,2}.

Vaginal discharge was the most common presenting symptom, reported by 78 (91.8%) participants. This finding is consistent with the established clinical presentation of vaginitis, in which abnormal vaginal discharge is one of the principal reasons for gynecological consultation. However, discharge is not specific for a particular etiology and may occur in bacterial vaginosis, vulvovaginal candidiasis, trichomoniasis and aerobic vaginitis^{1,3}. Current guidance emphasizes that clinical history alone is insufficient for accurate diagnosis in many women with vaginal symptoms and that examination and appropriate laboratory testing should be incorporated whenever feasible.

Vaginal itching was the second most frequent symptom in our study, occurring in 52 (61.2%) women. Pruritus is classically associated with vulvovaginal candidiasis, although it may also occur in bacterial and mixed vaginal disorders. The coexistence of itching with discharge therefore cannot be regarded as diagnostic of candidiasis without appropriate microbiological confirmation^{3,4}.

Foul-smelling discharge was reported by 38 (44.7%) women. An unpleasant or fishy odor is traditionally

associated with bacterial vaginosis and reflects changes in the vaginal microbial ecosystem and production of volatile amines.⁵ Nevertheless, odor alone is insufficient to establish a diagnosis of bacterial vaginosis because similar complaints may occur in other vaginal conditions. Standardized clinical and laboratory criteria therefore remain important.⁶

The character of discharge also varied considerably. White or whitish discharge was the most frequent type, followed by curdy/coagulated and yellowish discharge. White, curdy discharge is often associated with vulvovaginal candidiasis, whereas thin or malodorous discharge is more frequently associated with bacterial vaginosis. Frothy or yellow-green discharge may occur with trichomoniasis. However, these clinical associations are not absolute, and microbiological testing remains valuable when the diagnosis is uncertain^{7,8}.

The normal vaginal microbiota is predominantly composed of *Lactobacillus* species, which contribute to maintenance of vaginal acidity and protection against colonization by potentially pathogenic organisms. Disruption of this *Lactobacillus*-dominant environment may result in dysbiosis and predispose to bacterial vaginosis and other vaginal disorders⁹. The vaginal microbiome is now recognized as a dynamic ecosystem rather than a simple collection of individual organisms.

Bacterial vaginosis represents an important example of this microbial imbalance. Rather than being caused by a single pathogen, BV is associated with replacement of *Lactobacillus*-dominant communities by polymicrobial populations containing organisms such as *Gardnerella vaginalis*, *Fannyhessea vaginae*, *Prevotella* species and other anaerobic bacteria^{5,10}. This polymicrobial nature may explain why conventional culture alone does not always adequately characterize BV.

Vulvovaginal candidiasis is another important cause of symptomatic vaginitis. *Candida albicans* remains the most frequently recognized species, but non-*albicans* *Candida* species are increasingly encountered, particularly in recurrent or complicated infections. Species-level identification may therefore have clinical importance because antifungal susceptibility can vary between *Candida* species.^{11,12}

Trichomoniasis, caused by *Trichomonas vaginalis*, is an important sexually transmitted infection and may present with vaginal discharge, irritation and dysuria. However, some women remain asymptomatic, and the sensitivity of conventional microscopy is lower than that of nucleic acid amplification methods¹³. Consequently, failure to identify *T. vaginalis* clinically or by low-sensitivity testing may result in missed infections.

Aerobic bacterial organisms also contribute to symptomatic vaginal disease. Aerobic vaginitis has been associated with organisms including *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus* species and other aerobic bacteria¹⁴. The recognition of aerobic vaginitis is particularly relevant because its clinical and microscopic characteristics differ from those of bacterial vaginosis, despite overlapping symptoms.

The microbiological diversity observed in the present study supports the concept that vaginal symptoms constitute a heterogeneous clinical syndrome. A woman presenting with discharge and itching may have candidiasis, bacterial vaginosis, trichomoniasis, aerobic vaginitis, mixed infection or a noninfectious cause. Consequently, empirical treatment based only on symptoms may result in inappropriate antimicrobial or antifungal exposure¹⁵.

The 25.9% microbiological positivity rate observed in the corrected study dataset is an important finding. It

indicates that most symptomatic women in this study did not have a significant pathogen detected by the methods used. This may reflect the presence of physiological discharge, noninfectious causes of symptoms, limitations of conventional microbiological methods, or conditions not detected by the investigations performed. Therefore, a positive symptom history should not automatically be equated with confirmed infection.

Antimicrobial susceptibility testing is particularly relevant when bacterial pathogens are isolated. Increasing antimicrobial resistance has complicated the management of bacterial infections worldwide and reinforces the importance of selecting antimicrobial therapy according to microbiological findings whenever possible^{16,17}. Laboratory-guided therapy can reduce unnecessary antimicrobial exposure and contribute to antimicrobial stewardship.

The interpretation of *Candida* isolation also requires clinical correlation. *Candida* species may colonize the vagina without producing symptomatic disease, and therefore isolation alone does not necessarily establish vulvovaginal candidiasis^{11,12}. Clinical symptoms, examination findings and laboratory evidence should be interpreted together.

Recent Indian evidence provides useful comparison with the present study. Singh et al. (2025) evaluated 220 symptomatic women with cervicovaginal discharge and reported microbial growth in 77.27% of samples. Aerobic vaginitis was the most frequent category, followed by bacterial vaginosis, vulvovaginal candidiasis and trichomoniasis. *Enterococcus* species, *E. coli* and *S. aureus* were among the important aerobic organisms, while non-*albicans* *Candida* species were prominent among *Candida* isolates^{18,19}. This recent Indian evidence emphasizes the considerable heterogeneity of vaginal

infections and the importance of accurate organism identification.

Another recent Indian investigation evaluated diagnostic modalities for bacterial vaginosis and aerobic vaginitis and emphasized that these conditions may remain underdiagnosed when clinical assessment is not supported by appropriate laboratory methods.²⁰ These findings reinforce the relevance of microbiological evaluation in women with persistent or clinically ambiguous vaginal symptoms.

Contemporary research has increasingly focused on the vaginal microbiome rather than individual organisms. Brochu et al. (2025) characterized vaginal microbiomes in clinician-collected BV-diagnosed samples and demonstrated the complex microbial communities associated with BV.²¹ Such findings support the concept that BV represents a disturbance of the overall vaginal ecosystem rather than infection caused by a single microorganism.

Molecular approaches have further expanded the ability to characterize vaginal microbial communities. Oyenihni et al. (2024) developed a quantitative PCR approach targeting 22 BV-associated species and reported high analytical sensitivity and specificity for the targeted organisms. Their work illustrates the potential value of species-level and relative-abundance information in distinguishing BV-associated microbial states²².

Recent multi-omics research has explored combinations of microbiome and metabolomic markers for the diagnosis of bacterial vaginosis²³. Such approaches may eventually provide more objective and reproducible diagnostic models than conventional clinical criteria alone, although their availability and cost may limit routine implementation.

Artificial-intelligence-assisted and multiplex molecular approaches are also being investigated for vaginal microbiological diagnosis. Recent work has examined microbiota profiling for bacterial vaginosis, demonstrating the potential of molecular panels to detect multiple organisms and microbial patterns simultaneously²⁴. These approaches may be particularly useful in women with recurrent, atypical or clinically ambiguous symptoms.

Recent research has also highlighted that different molecular methods may produce differing microbiological classifications. A 2025 study comparing vaginal sequencing approaches demonstrated differences in microbiome characterization and BV-associated microbial profiles depending on the molecular methodology used²⁵. This observation is important because increasingly sensitive molecular tests may detect organisms that represent colonization or part of the normal microbial ecosystem rather than clinically significant infection.

The expanding role of molecular diagnostics does not eliminate the importance of conventional methods. Microscopy, Gram staining and culture remain valuable because they are relatively accessible, inexpensive and familiar to microbiology laboratories. In resource-limited settings, these methods may remain the principal diagnostic tools. Molecular methods should therefore be regarded as complementary approaches, particularly where conventional testing produces equivocal results.

Recent reviews have emphasized the potential of vaginal microbiome diagnostics to improve women's health but have also highlighted challenges relating to standardization, interpretation, cost and translation of research assays into routine clinical practice.²⁶ Thus, although advanced molecular techniques offer

considerable promise, clinical correlation remains essential.

Taken together, the findings of the present study and the available literature demonstrate that vaginal symptoms constitute a heterogeneous clinical syndrome. The predominance of vaginal discharge and itching in our participants is consistent with the recognized clinical presentation of vaginitis, while the relatively limited proportion of microbiologically confirmed infection emphasizes the need to distinguish infectious from noninfectious causes.

The present study also reinforces the importance of antimicrobial stewardship. Antimicrobial therapy should ideally be guided by the identified pathogen and susceptibility profile when bacterial infection is confirmed. Unnecessary empirical antibiotic exposure may contribute to resistance and may also disturb the normal vaginal microbiota.

In conclusion, a clinico-microbiological approach is preferable to symptom-based diagnosis alone. Conventional microscopy and culture remain important diagnostic tools, while molecular and microbiome-based methods may provide additional information in selected patients. Larger studies incorporating standardized diagnostic criteria, species-level identification, antimicrobial susceptibility testing and molecular methods are warranted to better define the microbiological spectrum of vaginal infections in the Indian population.

Conclusion

Vaginal discharge was the most common presenting symptom among the women studied, followed by vaginal itching and foul-smelling discharge. Among 85 symptomatic women, 22 (25.9%) showed microbiological evidence of vaginal infection, while 63

(74.1%) had no significant pathogen detected. The findings demonstrate that clinical symptoms alone may not reliably establish the etiology of vaginal infection. Microbiological examination is useful for differentiating bacterial, fungal and protozoal causes of vaginal symptoms. Antimicrobial susceptibility testing of clinically significant bacterial isolates can support rational and targeted antimicrobial therapy. A combined clinical and microbiological approach may help reduce inappropriate antimicrobial use and improve patient management.

Limitations

- The study had a relatively small sample size of 85 participants and was conducted at a single tertiary-care center, limiting generalizability.
- The observational design and limited follow-up prevented assessment of recurrence, treatment response and long-term antimicrobial resistance patterns.
- Molecular diagnostic methods were not routinely incorporated, which may have limited detection of some organisms.
- Species-level characterization of all isolates was limited by the available laboratory data.

Declarations

Conflicts of interest: There is no any conflict of interest associated with this study

Consent to participate: There is consent to participate.

Consent for publication: There is consent for the publication of this paper.

Author's contributions: Author equally contributed the work.

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